TERT promoter mutations occur frequently in gliomas and a subset of tumors derived from cells with low rates of self-renewal

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Contributed by Bert Vogelstein, February 26, 2013 (sent for review February 19, 2013)

Malignant cells, like all actively growing cells, must maintain their telomeres, but genetic mechanisms responsible for telomere maintenance in tumors have only recently been discovered. In particular, mutations of the telomere binding proteins *alpha thalassemia/mental retardation syndrome X-linked* (*ATRX*) or *death-domain associated protein* (*DAXX*) have been shown to underlie a telomere maintenance mechanism not involving telomerase (alternative lengthening of telomeres), and point mutations in the promoter of the *telomerase reverse transcriptase* (*TERT*) gene increase telomerase expression and have been shown to occur in melanomas and a small number of other tumors. To further define the tumor types in which this latter mechanism plays a role, we surveyed 1,230 tumors of 60 different types. We found that tumors could be divided into types with low (<15%) and high (≥15%) frequencies of *TERT* promoter mutations. The nine TERT-high tumor types almost always originated in tissues with relatively low rates of self renewal, including melanomas, liposarcomas, hepatocellular carcinomas, urothelial carcinomas, squamous cell carcinomas of the tongue, medulloblastomas, and subtypes of gliomas (including 83% of primary glioblastoma, the most common brain tumor type). *TERT* and *ATRX* mutations were mutually exclusive, suggesting that these two genetic mechanisms confer equivalent selective growth advantages. In addition to their implications for understanding the relationship between telomeres and tumorigenesis, *TERT* mutations provide a biomarker that may be useful for the early detection of urinary tract and liver tumors and aid in the classification and prognostication of brain tumors.

Telomeres are nucleoprotein complexes at the ends of eukaryotic chromosomes that are required for chromosomal integrity. Several hundred nucleotides of telomere repeats cap each chromosomal end, and in the absence of telomerase activity, telomeres shorten with each cell division (1). Eventually, uncapped telomeres trigger cell death or senescence. Cancer cells seem to divide ad infinitum and therefore, require some telomere maintenance mechanism to avoid this fate. Because telomerase activity is generally higher in cancer cells than normal cells, it was originally believed that telomerase was somehow activated in cancer cells (2–6). However, it was subsequently realized that telomerase was only inactive in terminally differentiated cells and that normal stem cells in self-renewing tissues retained telomerase activity (1, 7–9). Because normal stem cells must replicate throughout the long lifetimes of mammals (which can be more than a century in humans), it is clear that such cells must also retain telomerase activity. Because normal stem cells are thought to be the progenitors of cancers, there would be no need to specifically activate telomerase in cancer cells; the enzyme was already active in the precursors, just as were the hundreds of other enzymes and proteins normally required for cell proliferation.

This view was challenged by the discovery of another mechanism for maintaining telomere length [i.e., alternative lengthening of telomeres (ALT)] (10–12). ALT occurs in the absence of telomerase activity and seems to be dependent on homologous recombination. It occurs in a particularly high fraction of certain tumor types, such as sarcomas, pancreatic neuroendocrine tumors, and brain tumors, but rarely in most common tumor types, such as those tumor types of the colon, breast, lung, prostate, or pancreas (13). Why would cancer cells need ALT if telomerase activity was already constitutively active in their precursors? This question was highlighted by the discovery that many ALT cancers harbor mutations in *alpha thalassemia/mental retardation syndrome X-linked* (*ATRX*) or *death-domain associated protein* (*DAXX*), genes encoding proteins that interact with each other at telomeres (10, 11). Presumably, the absence of functional ATRX/DAXX complexes permits the homologous recombination resulting in ALT. At minimum, these data were compatible with the ideas that there could be a selective advantage for genetic alterations that results in telomere maintenance and that telomerase is not indefinitely activated in all normal stem cell precursors of cancers.

Another challenge to the idea that genetic alterations were not required for telomerase activation in cancer was raised by the finding that mutations of the *telomerase reverse transcriptase* (*TERT*) promoter occurred in ∼70% of melanomas and in a

Author contributions: P.J.K., Z.J.R., Y.J., C.B., B.V., and H.Y. designed research; P.J.K., Z.J.R., Y.J., C.B., and B.A.R. performed research; N.A., L.A.D., A.H.F., H.F., G.L.G., B.C.G., A.P.G., T.-C.H., Y.H., R.H.H., G.I.J., N.M., A.K.M., F.M., G.J.N., G.J.R., T.A.R., M.S., I.-M.S., D.T., M.S.T., V.E.V., T.-L.W., N.W., L.D.W., M.Z., R.E.M., D.D.B., N.P., K.W.K., B.V., and H.Y. contributed new reagents/analytic tools; P.J.K., Z.J.R., Y.J., C.B., B.A.R., R.E.M., N.P., K.W.K., B.V., and H.Y. analyzed data; and P.J.K., Z.J.R., Y.J., C.B., B.V., and H.Y. wrote the paper.

The authors declare no conflict of interest.

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1303607110/-/DCSupplemental.

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small number of tumor cell lines derived from various tissue types (14, 15). Importantly, only 5 of 110 cell lines derived from lung, stomach, ovary, uterus, or prostate cancers harbored *TERT* promoter mutations, whereas 19 mutations were found among 37 cell lines derived from various other tumor types. This situation is analogous to the situation for ALT, which is infrequently observed in common epithelial cancers but is observed more regularly in tumors derived from nonepithelial cells, particularly sarcomas and brain tumors (13).

These findings prompted us to formulate a hypothesis about the mechanisms responsible for telomerase activity in cancers. We suggest that there are two ways to maintain telomere lengths as cells divide: (*i*) through epigenetic regulation of telomerase activity, which occurs in stem cells of tissues that are rapidly renewing, and (*ii*) through somatic mutations that maintain telomere lengths, such as mutations in the *TERT* promoter or mutations in *DAXX* or *ATRX*. Those cancers that originate in tissues that are constantly self-renewing, such as cancers of the epithelia of the gastrointestinal tract and skin or bone marrow, would be unlikely to harbor telomere-maintaining mutations, because telomerase is already epigenetically activated in their precursor cells. In contrast, tumors arising from cells that are not constantly self-renewing, such as neurons, glial cells, fibroblasts, hepatocytes, islet cells, and pancreatic ductal epithelial cells, might frequently harbor such mutations. A corollary of this hypothesis is that tumor types exhibiting high frequencies of ALT would also exhibit high frequencies of *TERT* mutations, and these mutations would be distributed in a mutually exclusive fashion. To test these hypotheses as well as answer other questions related to the role of *TERT* promoter mutations in various cancer types, we determined the prevalence of *TERT* promoter mutations in a large number of tumors.

Results

We attempted to evaluate at least 20 individual specimens of common tumor types and fewer specimens of rare tumor types, depending on availability of specimens in our laboratories. In those tumor types in which our pilot studies showed a significant number of mutations, additional tumors were evaluated. Melanomas and tumors of the lung, stomach, and esophagus were excluded, because they had already been adequately evaluated in the seminal papers cited (14, 15). When primary tumors rather than cell lines were used, we ensured that the fraction of neoplastic cells was >50% through histopathologic examination of frozen sections of the tissue blocks used for DNA purification. In those cases in which the neoplastic content was <50%, we microdissected the lesions to enrich the neoplastic content to >50%. Primers were designed to amplify the region containing the two *TERT* mutations that were previously described—C228T and C250T—corresponding to the positions 124 and 146 bp, respectively, upstream of the *TERT* ATG start site (14, 15). The PCR fragments were then purified and analyzed by conventional Sanger sequencing.

In all, we evaluated *TERT* promoter mutations in 1,230 tumor specimens and identified 231 mutations (18.8%) (Table 1). C228T and C250T mutations accounted for 77.5% and 20.8% of the alterations, respectively (Dataset S1). Additionally, we detected four mutations that had not been observed previously: three C228A mutations and one C229A mutation (Dataset S1). All four of these mutations as well as a representative subset of the C228T and C250T mutations ($n = 59$) were somatic, as evidenced by their absence in normal tissues of the patients containing the mutations in their tumors.

The 1,230 tumors represented 60 tumor types. In 26 of these tumor types, at least 15 individual tumors were evaluated (comprising a total of 1,043 individual tumors) (Fig. 1). In the remaining tumor types, only a small number of samples (2–12) was available, in part because these tumor types are generally uncommon in Western populations (Table 1). Among the tumor types in which at least 15 individual tumors were available for study, a clear distinction could be made. Eighteen of these tumor types had only occasional *TERT* promoter mutations (zero to three mutations, comprising 0–15% of the tumors of each type) (Fig. 1). We classified these tumor types as TERT-low (TERT-L), because they had a low frequency of *TERT* promoter mutations. Eight other tumor types were classified as TERT-high (TERT-H) because of their relatively high prevalence of *TERT* promoter mutations (16–83% of the tumors of each type).

The TERT-L tumor types included some of the most prevalent cancers, including epithelial tumors of the breast, prostate, thyroid, pancreas, gall bladder, uterus, and colon (as well as tumors of the lung, stomach, and esophagus based on prior studies) (14, 15) and leukemias. In fact, no *TERT* mutations were identified in any specimen of 30 tumor types that we studied, comprising a total of 546 tumors (Table 1). Some nonepithelial cancers, such as synovial sarcomas, chordomas, neuroblastomas, osteosarcomas, and ependymomas, were also TERT-L.

Eight TERT-H tumor types were identified (in addition to the previously described melanomas) (14, 15). These tumors included tumors of the CNS, transitional cell carcinomas of the urinary tract, hepatocellular carcinomas, myxoid liposarcomas, and oral cavity carcinomas. Although only a small number of TERT-H tumors (other than melanomas) were examined in previous studies (15), mutations in gliomas, hepatocellular, and oral cavity carcinomas were detected, which would be expected on the basis of the high frequency of mutation in these tumors types (Table 1).

Table 1. Frequency of *TERT* promoter mutations

Tumor type*	No. tumors	No. tumors mutated (%)
Chondrosarcoma	2	1 (50)
Dysembryoplastic neuroepithelial tumor	3	1 (33.3)
Endometrial cancer	19	2 (10.5)
Ependymoma	36	1 (2.7)
Fibrosarcoma	3	1 (33.3)
Glioma†	223	114 (51.1)
Hepatocellular carcinoma	61	27 (44.2)
Medulloblastoma	91	19 (20.8)
Myxofibrosarcoma	10	1 (10.0)
Myxoid liposarcoma	24	19 (79.1)
Neuroblastoma	22	2 (9)
Osteosarcoma	23	1 (4.3)
Ovarian, clear cell carcinoma	12	2 (16.6)
Ovarian, low grade serous	8	1 (12.5)
Solitary fibrous tumor (SFT)	10	2 (20.0)
Squamous cell carcinoma of head and neck	70	12 (17.1)
Squamous cell carcinoma of the cervix	22	1 (4.5)
Squamous cell carcinoma of the skin	5	1 (20)
Urothelial carcinoma of bladder	21	14 (66.6)
Urothelial carcinoma of upper urinary epithelium	19	9 (47.3)

*No mutations were found in acute myeloid leukemia ($n = 48$), alveolar rhabdomyosarcoma ($n = 7$), atypical lipomatous tumor ($n = 10$), breast carcinoma ($n = 88$), cholangiosarcoma ($n = 28$), central/conventional chondrosarcoma ($n = 9$), chronic lympoid leukemia ($n = 15$), chronic myeloid leukemia ($n = 6$), colorectal adenocarcinoma ($n = 22$), embryonal rhabdomyosarcoma ($n = 8$), esthesioneuroblastoma ($n = 11$), extraskeletal myxoid chondrosarcoma ($n = 3$), fibrolammellar carcinoma of the liver ($n = 12$), gall bladder carcinoma ($n = 10$), gastrointestinal stromal tumor ($n = 9$), hepatoblastoma ($n = 3$), leiomyosarcoma ($n = 3$), conventional lipoma ($n = 8$), low grade fibromyxoid sarcoma ($n = 9$), malignant peripheral nerve sheath tumor ($n = 3$), medullary thyroid carcinoma ($n = 24$), meningioma ($n = 20$), mesothelioma ($n = 4$), pancreatic acinar carcinoma ($n = 25$), pancreatic ductal adenocarcinoma ($n = 24$), pancreatic neuroendocrine tumor ($n = 68$), prostate carcinoma ($n = 34$), spinal ependymoma ($n = 9$), synovial sarcoma ($n = 16$), or undifferentiated pleomorphic soft tissue sarcoma ($n = 10$) samples.
†Glioma comprises 11 subtypes; see Dataset S1 and Table S3.

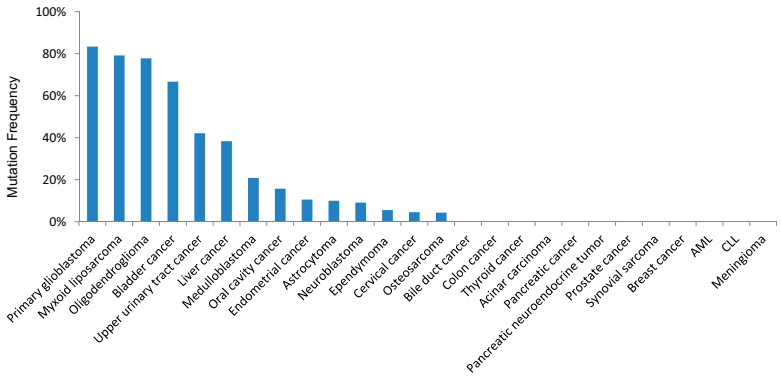

Fig. 1. Frequency of *TERT* promoter mutations; 15 or more tumors were analyzed in 26 tumor types. Gliomas are divided into primary GBM, astrocytoma (including astrocytoma grades II and III, as well as secondary GBM), and oligodendroglioma.

Clinical and Molecular Correlations in TERT-H Tumors. ***Sarcomas.*** One of the highest frequencies of *TERT* promoter mutation was found in myxoid liposarcoma (19 of 24 tumors, 79% with mutation). Myxoid liposarcomas account for more than one-third of all liposarcomas and ∼10% of all adult soft tissue sarcomas (16). Patients are relatively young, with a peak age range between 30 and 50 y. At the genetic level, the most characteristic change is a *t*(12;16) (q13;p11) chromosomal translocation that results in the fusion of the *FUS* and *DDIT3* genes (16, 17). The cellular origin of these tumors is unknown, but preadipocytic progenitor cells and mesenchymal stem cells have been implicated (18); after embryogenesis, the mitotic activity of these cells is thought to be low. Other sarcomas, also thought to originate from mesenchymal cells that do not self-renew in the absence of damage, were not TERT-H (Table 1). These sarcomas included synovial sarcomas (0% of 16 tumors) and osteosarcomas (4.3% of 23 tumors). Of note, myxoid liposarcomas have been previously shown to have a relatively high prevalence of ALT (24% of 38 tumors) (13, 19). The data, in aggregate, are compatible with the idea that myxoid liposarcomas almost always genetically activate telomere maintenance genes through either *TERT* promoter mutations or ALT.

Hepatocellular carcinomas. Hepatocellular carcinomas (HCCs) are the third leading cause of cancer mortality worldwide, and their incidence is increasing in the United States (20). Most HCCs in the United States are associated with Hepatitis B or C Virus infection, whereas others are associated with alcoholic cirrhosis; 44% of HCC samples that we evaluated harbored *TERT* promoter mutations (27/61). This finding makes *TERT* the most commonly mutated gene yet observed in this tumor type (21, 22). The mutations seemed to occur relatively early in tumorigenesis, because they were observed in 39% of stage I well-differentiated HCCs (Table S1). *TERT* mutations were observed in virally associated tumors as well as cases without any underlying liver disease at similar frequencies (Table S1). There was also no difference in the prevalence of *TERT* promoter mutations with respect to sex, age, or ethnicity (Table S1). ALT has been observed in 7% of 121 HCCs studied previously (13).

Urinary tract cancers. Urothelial carcinoma of the bladder is the fourth most common type of cancer in American males. In 2013, over 73,000 patients will be diagnosed with bladder cancer leading to approximately 15,000 deaths in the US alone (23). Two-thirds of the 21 urothelial carcinomas of the bladder that we studied harbored *TERT* promoter mutations. We were also able to evaluate 19 urothelial carcinomas of the upper urinary tract, a much less common anatomic site for this histopathologic subtype of tumor. Nine of nineteen upper urinary tract urothelial carcinomas harbored *TERT* mutations. *TERT* mutations are, therefore, the most frequently mutated genes yet identified in urothelial carcinoma of either the bladder or upper urinary tract (24). The prevalence of ALT in bladder cancers is very low (1% of 188 cancers) (13).

Head and neck cancers. Head and neck cancers are almost always squamous cell carcinomas and can occur throughout the oral cavity lining (mucous membranes of the cheek, hard and soft palate, tongue, supraglottis, etc.). It is the sixth most common cancer in the world, and 50,000 cases occurred in the United States in 2012. We identified *TERT* promoter mutations in 17% of 70 oral cavity cancers that we evaluated. However, the anatomic distribution of the cases with *TERT* promoter mutations was striking: 11 of 12 cancers with *TERT* promoter mutations were in the oral tongue, although only 23 of 70 total cases originated in the oral tongue ($P < 0.0001$, Fisher exact probability test, two-tailed) (Table S2). The basis for this extraordinary selectivity is curious given the shared characteristics of the squamous epithelium lining the tongue and other parts of the head and neck, including the oral cavity. Moreover, we evaluated 22 squamous cell carcinomas of another site (the cervix) and found only one *TERT* mutation (4.5%) (Table 1). Most cervical squamous cell carcinomas and a subset of head and neck squamous cell carcinomas are caused by human papillomavirus, which can activate telomerase by expressing E6 and E7 viral oncogenes (25). These findings raise the possibility that human papillomavirus infection and *TERT* mutation may be alternative mechanisms to activate telomerase among squamous cell carcinomas. We were unable to test correlations between TERT promoter mutations and HPV status or other clinical parameters because of the small number of patients with available data (Table S2). There have been no ALT cases identified among 70 head and neck cancers, including 41 oral cavity cancers (13).

Medulloblastomas. Medulloblastoma is the most common malignant brain tumor of childhood (26). *TERT* mutations occurred in 21% of 91 medulloblastomas that we evaluated. As with the oral cavity cancers, *TERT* mutations were not distributed randomly among the medulloblastoma patients. Although medulloblastomas are usually diagnosed at a young age, those medulloblastomas with *TERT* mutations were diagnosed at a considerably older age (median = 6 vs. 16 y, $P = 0.0012$, *t* test assuming unequal variances, two-tailed) (Fig. S1*A*). This observation has important implications for understanding the basis for the selectivity of the tumor types harboring *TERT* promoter mutations (*Discussion*); 45 of 90 patients had been assessed previously for *orthodenticle homeobox 2* (*OTX2*) gene amplification and expression, and alterations in this transcription factor are known to correlate with clinically distinct molecular subtypes of medulloblastoma (27). *OTX2* expression was >100-fold higher in medulloblastoma patients without *TERT* promoter mutations than in those patients with *TERT* promoter mutations (note the log scale in Fig. S1*B*). The high levels of OTX2 expression were usually the result of OTX2 gene amplification (Fig. S1*C*). The association of *TERT* promoter mutations with an older age at diagnosis and a lack of *OTX2* overexpression raises the possibility that *TERT* mutations occur in a specific clinical and molecular subtype of medulloblastoma. The most likely molecular subtype of medulloblastoma that may be enriched for *TERT* mutations is the noninfant sonic hedgehog subtype, which is characterized by an older age at diagnosis and lower expression of *OTX2* (28, 29). Larger studies will be needed to make

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this association more definitive. ALT has been observed in 7% of 55 medulloblastomas studied previously (13).

Gliomas. Gliomas are the most common CNS tumor type and accounted for >14,000 deaths in the United States last year (30). Histopathological and clinical criteria established by the World Health Organization are used to characterize these tumors into several subtypes (30). We considered the four main subtypes individually (Table S3).

Primary glioblastoma. These primary glioblastomas (GBMs) are the most common malignant brain tumors in adults, accounting for ~17% of all intracranial tumors, and they confer the worst survival (median of ~15 mo) (31). These high-grade (grade IV) tumors have no detectable precursor lesions and have been referred to as de novo tumors. The prevalence of *TERT* promoter mutations was remarkably high in GBMs of adults (83% of 78 tumors) (Table S3). This prevalence is higher than the prevalence of any other genetic mutation in this tumor type (32). These findings provide a molecular mechanism responsible for the high levels of *TERT* mRNA and telomerase activity observed in GBMs (33).

For 51 of 78 primary GBM tumors, data on other common genetic alterations as well as clinical data were available (Fig. 2*A*). Interestingly, *EGFR* amplification, a classic molecular feature of primary GBM, exclusively occurred in tumors with *TERT* mutations ($P = 0.0006$, Fisher exact probability test, two-tailed).

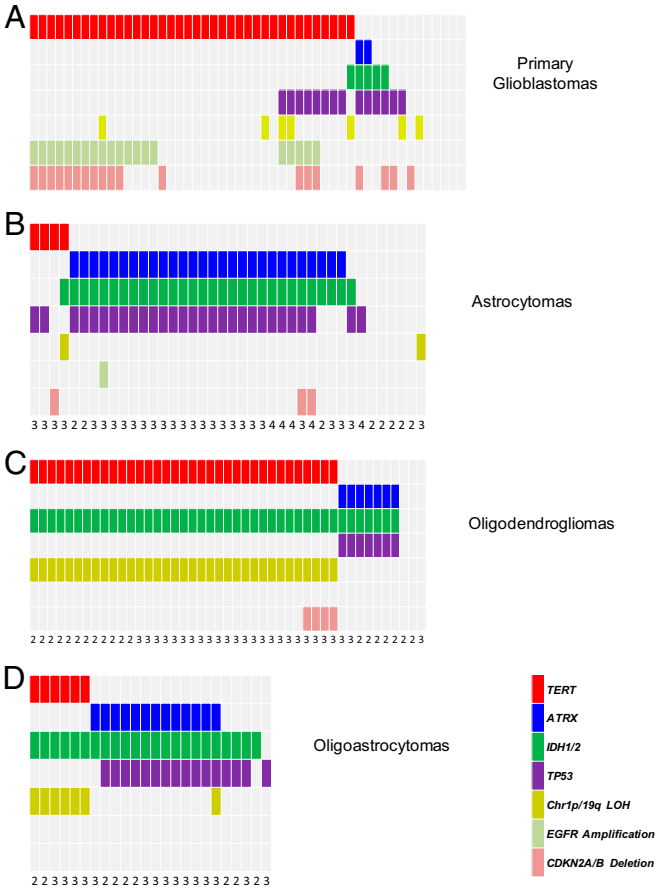

Fig. 2. Mutations of selected genes in glioma subtypes. (*A*) Distribution of *TERT* mutations and other genetic events in 51 primary GBMs. (*B*) Distribution of *TERT* mutations and other genetic events among 40 astrocytomas, including grades II–III astrocytomas and grade IV secondary GBMs. (*C*) Distribution of *TERT* mutations and other genetic events among 45 oligodendrogliomas. (*D*) Distribution of *TERT* mutations and other genetic events among 24 oligoastrocytomas. World Health Organization tumor grade is indicated under each column. Light gray cells denote WT status in tumors.

Conversely, no association was identified between *TERT* mutation and either *TP53* mutation or *CDKN2A* deletion. Importantly, the frequency of *TERT* promoter mutations was considerably less in primary GBMs of pediatric patients (11% of 19 tumors) than adult patients (*Discussion*) (Table S3). ALT was observed in 11% of 105 adult GBM and 44% of pediatric GBM (i.e., the reverse of the pattern observed for *TERT* promoter mutations) (13). Primary GBM patients without *TERT* mutations survived considerably longer, on average, than patients with such mutations (median = 27 vs. 14 mo, $P = 0.01$ by the log rank test) (Fig. S3).

Astrocytomas. Infiltrative astrocytic tumors frequently progress, with recurrent lesions often of higher grade than the original lesions excised at surgery. They are most often grade II or III but can progress to grade IV (at which point they are often termed secondary GBMs). Astrocytomas of any stage rarely contained *TERT* promoter mutations (10% of 40 total samples) (Table S3). Instead, they more frequently contained *isocitrate dehydrogenase 1* (*IDH1*) or *isocitrate dehydrogenase 2* (*IDH2*) mutations (75% of 40 tumors), *ATRX* mutations (70% of 40 tumors), and *TP53* mutations (73% of 40 tumors) (Fig. 2*B*). ALT has been observed in 63% of 57 astrocytomas, consistent with the high prevalence of *ATRX* mutations (13). The lack of activating *TERT* mutations in *IDH1* mutant tumors is also corroborated by the lack of *TERT* mRNA and telomerase activity observed in these lesions (33).

Oligodendrogliomas. Like astrocytomas, oligodendrogliomas often progress, and they frequently contain *TERT* promoter mutations (78% of 45 tumor samples) (Table S3). Oligodendroglioma was the only tumor type studied (of all types, including non-CNS tumors) (Dataset S1) in which C250T mutations were nearly as frequent as C228T mutations. In oligodendrogliomas, 43% of tumors with *TERT* mutations contained C250T substitutions, whereas in other gliomas, only 10% did ($P < 0.001$, Fisher exact probability test, two-tailed). Interestingly, 91% of 45 oligodendrogliomas that were evaluated for *ATRX* and *TERT* sequence alterations contained either an *ATRX* coding or a *TERT* promoter mutation, suggesting that genetic alterations resulting in telomere maintenance are required for tumorigenesis of this subtype.

Oligodendrogliomas have long been known to contain characteristic losses of chromosome arms 1p and 19q, and these losses reflect inactivation of the *CIC* gene on chromosome 19q and in some cases, inactivation of the *FUBP1* gene on chromosome 1p (34–36). Accordingly, 78% of 45 oligodendrogliomas contained chromosome arm 1p or 19q losses of heterozygosity (Fig. 2*C*) (34–36). Moreover, nearly all of them contained *IDH1* or *IDH2* mutations (93%).

Oligoastrocytomas. As their name implies, these tumors are mixed, with histologic features of both oligodendrogliomas and astrocytomas. This mixture, in part, reflects the difficulties in distinguishing the various glioma subtypes from one another on the basis of histopathologic or clinical criteria (37). The genetic features of this tumor subtype reflect this mixture: the prevalence of *TERT* promoter mutations (25% of 24 tumors) was intermediate between oligodendrogliomas and astrocytomas, as were the frequencies of chromosome (Chr) 1p/19q losses and *IDH1*/*2*, *TP53*, and *ATRX* mutations (Fig. 2*D*).

ALT Vs. TERT. ALT has been observed in tumors of the CNS (particularly gliomas) more frequently than tumors of any other tissue type. Given that *TERT* promoter mutations are also common in gliomas, the relationship between these two features could be determined with high confidence. The tumors depicted in Fig. 2 had previously been evaluated for alterations in *ATRX*, which is a nearly perfect surrogate for the ALT phenotype (11, 37). Our data show that there were 50 gliomas with *ATRX* mutations and 83 gliomas with *TERT* mutations; 0 of 83 tumors with *TERT* mutations contained *ATRX* mutations ($P < 0.0001$, Fisher exact probability test, two-tailed).

Discussion

The results described above, as well as the results published in refs. 14 and 15, provide evidence that supports one of the hypotheses raised in the Introduction and refutes others. The first of these hypotheses was that *TERT* mutations would only be observed in tumors derived from tissues that are not constantly self-renewing under normal circumstances. This hypothesis was supported in part: the vast majority of *TERT* promoter mutations occurred in tumors derived from tissues that do not continually self-renew. The TERT-H tumor types include only melanomas, certain subtypes of glioma, medulloblastomas, squamous cell cancers of the tongue, liposarcomas, HCCs, and urinary tract cancers. The normal transitional cells of the urinary tract have very low proliferative indices ($0.64\% \pm 0.52\%$), much lower than indices of gastrointestinal tract, bone marrow, or skin (38). Normal hepatocytes also do not turnover often (39), and glial cells are thought to have limited capacity for self-renewal (40).

Two other observations also support the hypothesis. Pediatric primary GBMs rarely contained *TERT* mutations (11%), whereas adult primary GBMs frequently did (83%). Pediatric GBMs are presumably derived from cells that are still dividing at the time of tumor initiation, and therefore, there is no selective advantage conferred by activating telomerase through a genetic mutation. Adult GBMs, in contrast, are presumably derived from postmitotic cells, and they should require telomerase activation. Similarly, medulloblastomas are embryonal tumors that typically arise from precursor cells with high self-renewal rates that do not usually persist in adults. This finding is consistent with our observation that the mean age of medulloblastoma patients with *TERT* mutations was considerably older than the mean age of medulloblastoma patients without *TERT* mutations (Fig. S1*A*).

There are, however, exceptions that belie the hypothesis that *TERT* mutations occur only in non–self-renewing tissues. The epithelium that lines the tongue constantly self-renews, but many squamous carcinomas of the tongue harbored *TERT* mutations (Table S2). Additionally, the squamous epithelia of the tongue certainly would not be expected to self-renew less than other squamous epithelia of the oral cavity, but the latter rarely harbored *TERT* mutations (Table S2). This finding may suggest that squamous carcinomas of the tongue originate from a different cell of origin than other oral cavity squamous carcinomas. Conversely, only a subset of the tumor types derived from non–self-renewing tissues was TERT-H. For example, the TERT-H tumors included myxoid liposarcomas but not synovial sarcomas. Moreover, cells of the pancreas (the islets of Langerhans and the ductal epithelial cells) rarely renew, but pancreatic tumors of all types (pancreatic neuroendocrine tumors, acinar carcinomas, and pancreatic ductal adenocarcinomas) were all TERT-L. The most that we can conclude at present is that non–self-renewing cell types are the major sources of TERT-H tumors but that non–self-renewal is only one of the factors that determines whether tumor cells with *TERT* promoter mutations will have a selective growth advantage over adjoining cells.

The first corollary to the hypothesis raised in the Introduction was that tumor types that displayed ALT would be those types that harbored *TERT* promoter mutations. This corollary is soundly refuted by these data, at least in general terms. Although tumor types of the CNS and liposarcomas had high frequencies of ALT as well as high frequencies of *TERT* promoter mutations, these tumor types were the exceptions rather than the rule. For example, pancreatic neuroendocrine tumors have very high frequencies of ALT but no evidence of *TERT* mutations. Conversely, bladder cancers frequently have *TERT* mutations but never have ALT (13). Additionally, even among gliomas, pediatric GBMs have high frequencies of ALT and low frequencies of *TERT* mutations, whereas adult GBMs have the reverse pattern.

The second corollary was that the selective advantage afforded by *TERT* mutation would be equivalent to the advantage afforded by *ATRX* mutation (conferring ALT). This hypothesis was most effectively tested in gliomas, in which both *ATRX* coding and *TERT* promoter mutations were common. There was a striking mutual exclusivity with respect to *ATRX* and *TERT* mutations ($P < 0.0001$), lending strong support to this idea.

These results also raise many unanswered questions. In some tumor types, such as gliomas, we can imagine that all tumors have genetically activated telomere maintenance programs through mutations in either *TERT* or *ATRX*. However, in other tumor types with frequent *ATRX* mutations, such as pancreatic neuroendocrine tumors, what is responsible for activating telomerase in the fraction of cases not exhibiting ALT if it is not a mutation in the *TERT* promoter? Similarly, what is responsible for activating telomerase in those tumors derived from non–self-renewing cell types in which neither ALT nor *TERT* mutations is frequently observed, such as synovial sarcomas or osteosarcomas? Also, there are occasional individual tumors among the TERT-L types that have *TERT* promoter mutations (e.g., cervical cancers, ovarian cancers, and in ref. 15, lung cancers). What distinguishes these occasional cancers from others of the same histopathologic subtype? Whole-genome sequencing studies, rather than those studies limited to the exome, might provide answers to these questions.

The results recorded here have practical as well as basic scientific implications. Two-thirds of bladder cancers had *TERT* promoter mutations, making it the most commonly mutated gene yet identified in invasive urothelial carcinoma of the bladder. Given the persistently high mortality rate despite multimodality treatment in this group of patients, these mutations represent ideal urinary biomarkers to detect bladder cancers at an early stage and to follow patients for evidence of progression or recurrence once they have been diagnosed (41). Similarly, the high prevalence of *TERT* promoter mutations in HCCs and glioma subtypes provides excellent candidate biomarkers for early detection (HCC) or monitoring (HCC in the plasma and gliomas in the cerebrospinal fluid) (42, 43).

Another practical implication involves diagnostics. We conjecture that tumors with *TERT* promoter or *ATRX* mutations are derived from different precursor cells and that either type of precursor cell is different from those types that are the precursors of tumors without such mutations. This distinction could aid classification of the tumors in clinically meaningful ways. For example, Fig. 2 and Fig. S2 outline the major genetic alterations occurring in the three most common types of gliomas. On the basis of the data in Fig. 2 *A*–*C*, we speculate that oligodendrogliomas that lack *TERT* mutations but contain *ATRX* mutations may behave more like astrocytomas than oligodendrogliomas and vice versa. Similarly, the primary GBMs without *TERT* mutations (15% of the total) may behave more like advanced progressive astrocytomas, which generally lack *TERT* mutations. This possibility is supported by the observation that those primary GBM patients without *TERT* mutations had a longer survival, on average, than other primary GBM patients (Fig. S3).

Methods

All clinical information and tissue were obtained with consent and Institutional Review Board approval from the various institutions donating material to this study, and they were obtained in accordance with the Health Insurance Portability and Accountability Act. Tissue sections were reviewed by board-certified pathologists to ensure that ≥50% of the cells used for DNA purification were neoplastic and confirm histopathological diagnosis. Oligonucleotides with the sequences 5′-M13-GGCCGATTCGACCTCTCT-3′ and 5′-AGCACCTCGCGGTAGTGG-3′, where M13 is a universal sequencing priming site with sequence 5′-tgtaaaacgacggccagt-3′, were used to PCR-amplify the proximal TERT promoter containing C228 and C250 (chr5: 1,295,228; chr5: 1,295,250, respectively; hg19) for Sanger sequencing using standard methods (44). Primary GBM copy number data as well as ALT status were derived from the data published in refs. 37, 45, and 46, and OTX2 copy number expression was derived from the data published in ref. 27. Brain tumor patients were treated at the Tisch Brain Tumor Center at Duke. For the purposes of this study, secondary GBM designates a GBM that was resected >1 y after a prior diagnosis of a lower-grade glioma (grades I–III), and all other GBMs were considered to be primary GBMs. Pediatric GBM samples were defined as those samples occurring before 21 y of age.

ACKNOWLEDGMENTS. We thank Lisa J. Ehinger and Diane L. Satterfield for collecting clinical samples. We also thank David Lister for 1p/19q analysis and J. Ptak, N. Silliman, L. Dobbyn, B. Bartlett, and J. Schaeffer for expert technical assistance. This project was supported by American Cancer Society Research Scholar Award RSG-10-126-01-CCE, National Cancer Institute Grant 5R01-CA140316, a Pediatric Brain Tumor Foundation Institute grant, a Voices Against Brain Cancer Foundation grant, a James S. McDonnell Foundation grant, The V Foundation, an Accelerate Brain Cancer Cure Foundation grant, The Burroughs Wellcome Career Award for Medical Scientists, The Johns Hopkins Clinician Scientist Award, a BSi Brain Science Translational Research grant, Malia's Cord Foundation Grant, The Zickler Family Foundation, Swim Across America, The Swedish Childhood Cancer Foundation, The Flight Attendant Medical Research Institute (FAMRI), FAMRI Clinical Innovator Award 2009, The Lustgarten Foundation, The Sol Goldman Pancreatic Cancer Research Center, and The Virginia and D. K. Ludwig Fund for Cancer Research. This work was also supported by the following National Institutes of Health Grants: Intramural Research Program of the National Cancer Institute, National Institute of Neurological Disorders and Stroke Grant 5P50 NS20023, National Cancer Institute Specialized Program of Research Excellence Grants 5P50 CA108785, CA121113, CA075115, CA104106, CA057345, CA129825, CA43460, CA57345, CA62924, P50DE019032, and ES04068, and CA172380, National Cancer Institute Contract N01-CN-43309, and National Cancer Institute Merit Award R37 011898.

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Supporting Information

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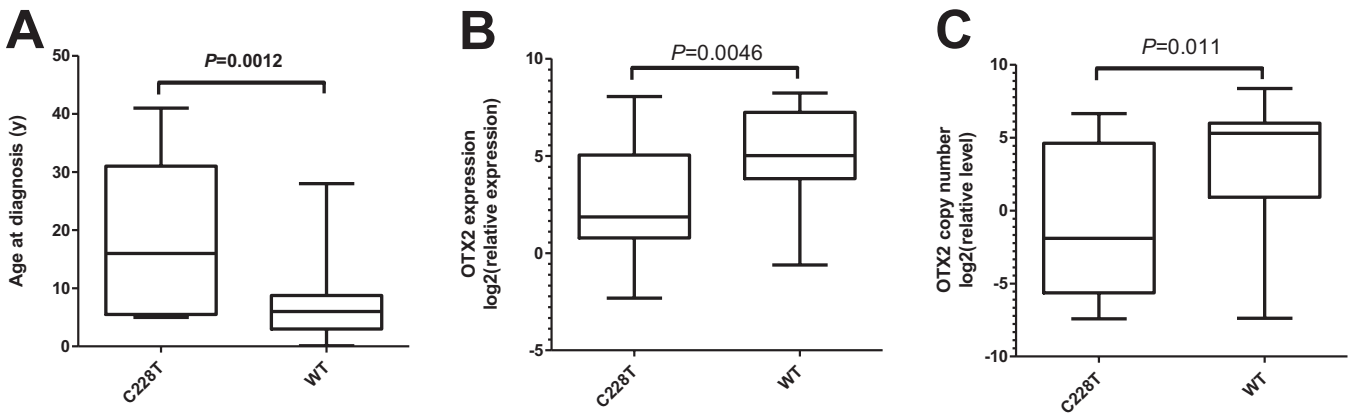


Fig. S1. *Telomerase reverse transcriptase* (*TERT*) promoter mutations and clinical characteristics of medulloblastomas. (*A*) Age at diagnosis of medulloblastoma patients with and without tumoral *TERT* promoter mutations. (*B*) Relative tumoral OTX2 expression, which was assessed by quantitative PCR, among patients with *TERT*-mutated and non–*TERT*-mutated tumors. (*C*) Relative tumoral OTX2 copy number, which was assessed by quantitative PCR, among patients with *TERT*-mutated and non–*TERT*-mutated tumors.

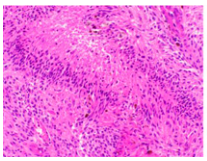
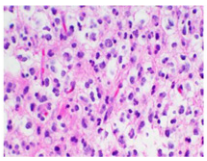
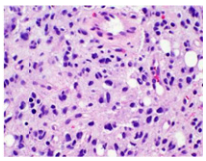
	Primary Glioblastoma	Oligodendroglioma	Progressive Astrocytoma
			
WHO Grade	IV	II-III	II-IV
TERT & IDH status	*TERT* mutant, *IDH1/2* wild type	*TERT* mutant, *IDH1/2* mutant	*TERT* wild type, *IDH1/2* mutant
Telomere Maintenance Mechanism	*TERT* Mutation	*TERT* Mutation	Alternative lengthening of telomeres
Other Frequent Molecular Alterations	*EGFR* amplification *CDKN2A/CDKN2B* deletion	*1p/19q* loss *CIC* mutation *FUBP1* mutation	*TP53* mutation *ATRX* mutation

Fig. S2. *Isocitrate dehydrogenase 1* (*IDH1*) and *TERT* mutations delineate oligodendrogliomas, primary glioblastomas (GBMs), and progressive astrocytomas. *TERT* promoter combined with *IDH1* mutational status allow for refinement of the classification of the three most common types of gliomas. World Health Organization (WHO) grade, typical *TERT* promoter and *IDH1* mutational status, telomere maintenance mechanism, and other frequent molecular alterations are shown for each group of tumors.

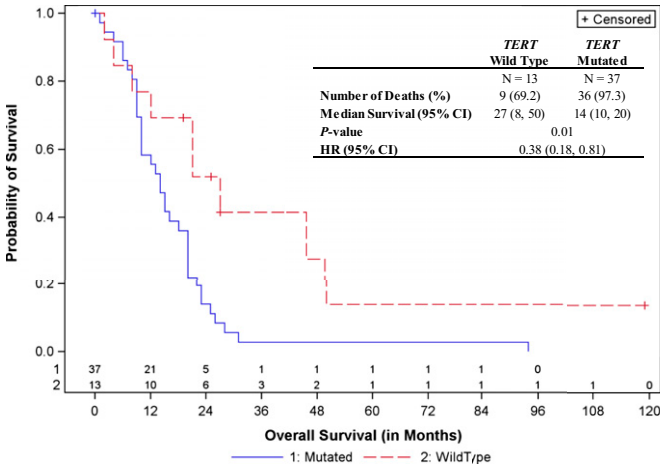


Fig. S3. Survival of primary GBM patients with *TERT* promoter-mutated tumors. Kaplan–Meier analysis of 50 primary GBM patients stratified by *TERT* promoter mutational status. Patients with *TERT* promoter WT tumors ($n = 13$) survived longer than patients with *TERT* promoter-mutated tumors ($n = 37$); median survival was 27 mo among the patients with *TERT* promoter WT tumors compared with 14 mo among patients with *TERT* promoter-mutated tumors. The estimated hazard ratio was 0.38 (95% confidence interval = 0.18, 0.81; $P = 0.01$, log rank test).

Table S1. Hepatocellular carcinoma patient data

Sample ID	Age (y)	Race	Sex	Stage	Differentiation	Focality	Underlying liver disease	Largest tumor size (cm)	Mutations in known drivers	*TERT* status
RK66	77	W	F	T2	Moderate	Single	HCV	4.5	CTNNB1	C228T
RK67	57	W	M	T1	Moderate	Single	HCV	3.5		WT
RK113	71	B	F	T2	Well	Multifocal	HCV	2.8	CTNNB1, ARID2	C228T
RK142	67	W	M	T2	Poor	Single	HCV	7.2	TP53	C228T
RK148	66	B	M	T1	Well	Single	HCV	4.5	CTNNB1, ARID2	C228T
RK153	58	W	F	T2	Well	Multifocal	HCV	2.8	CTNNB1, ARID2	C228T
RK168	62	B	F	T1	Well	Single	HCV	1.8		WT
RK179	62	W	M	T2	Poor	Multifocal	HCV	5.5	CTNNB1	C228T
RK183	65	B	F	T3b	Moderate	Multifocal	HCV	7.5	TP53	C228T
RK190	66	W	M	T1	Well	Single	HCV	1.6	TP53	WT
RK191	61	B	M	T2	Moderate	Multifocal	HCV	3.5	TP53	C228T
6700T	79	B	M	T1	Moderate	Single	HCV	4	ARID2	C228T
HCC 41 PT	67	UNK	M	UNK	Moderate	UNK	HBV	3.9		WT
HCC 42 PT	55	UNK	M	UNK	Moderate	UNK	HBV	1.7		WT
HCC 43 PT	64	UNK	M	UNK	Moderate	UNK	HBV	8		WT
HCC 45 PT	49	UNK	F	UNK	Poor	UNK	HCV	4		WT
HCC 46 PT	54	UNK	M	UNK	UNK	UNK	HBV	11	TP53	C228T
HCC 47 PT	53	UNK	M	UNK	UNK	UNK	HCV	1.3	ARID2	C228T
HCC 48 PT	48	UNK	M	UNK	Poor	UNK	HBV and ETOH	9		C228T
HCC 196	55	B	F	T1	Moderate	Single	HCV	1.8		WT
HCC 193	77	W	F	T2	Poor	Single	None	18		WT
HCC 192	60	W	F	T2	Moderate	Single	Cryptotenic liver disease	10	CTNNB1, ARID2	C228T
HCC 334	63	Asian	M	T1	Moderate	Single	HBV	3.4		WT
HCC 395	80	W	M	T1	Well	Single	None	6		C228T
HCC 712	61	W	M	T1	Moderate	Single	HCV	1.6		WT
RK3	59	W	M	T1	Well	Single	None	11	CTNNB1	C228T
RK5	70	W	M	T1	Moderate	Single	None	6.5	CTNNB1	C228T
RK9	40	W	F	T2	Moderate	Single	None	3.7		WT
RK15	59	Asian	F	T2	Moderate	Two	HBV	2.5		WT
RK63	63	B	M	T2	Moderate	Two	ETOH	5		C228T
RK65	55	W	M	T1	Well	Single	None	17		WT
RK69	71	W	M	T2	Moderate	Single	None	4.4		WT
RK73	65	B	M	T2	Moderate	Single	HBV	3.5		C228T
RK110	62	W	M	T1	Moderate	Single	ETOH	2		C228T
RK111	33	W	F	T1	Well	Single	Hepatic adenoma	1		WT
RK112	50	B	F	T2	Well	Single	None	9	TP53	WT
RK117	47	W	F	T2	Moderate	Single	None	15		WT
RK124	19	B	F	T3A	Moderate	Diffuse	None	Diffuse		C228T
RK129	45	W	F	t1	Well	Single	None	5		C228T
RK132	76	Asian	M	T1	Well	Single	HBV	4	TP53	WT
RK134	69	Asian	M	T1	Moderate	Single	None	3.2		C228T
RK139	74	W	M	T1	Moderate	Single	None	4.5		C228T
RK150	37	B	M	T2	Poor	Two	HBV	7		WT
RK165	46	Asian	M	T2	Poor	Single	HBV	5	TP53	C228T
RK166	65	Asian	F	T1	Moderate	Single	HBV	3	TP53	WT
RK174	60	W	M	T1	Moderate	Single	None	12	CTNNB1	WT
RK176	64	W	F	T1	Moderate	Single	None	8		WT
RK177	52	Asian	M	T1	Moderate	Single	HBV	1.2		WT
RK184	74	W	F	T2	Well	Two	None	5.3		C228T
RK193	73	Asian	M	T2	Moderate	Single	HBV	5.4		WT
RK194	76	W	M	T1	Well	Single	HBV	2.5	CTNNB1	WT

Only hepatocellular carcinoma (HCC) patients for which clinical information is known are tabulated. ETOH, alcohol; F, female; HBV, hepatitis B virus; HCV, hepatitis C virus; M, male; UNK, unknown; W, white; B, black.

Table S2. Oral cavity cancer patient data

Sample ID	Age (y)	Sex	Site/subsite	Histology	HPV status	Tobacco use	Mutations in known drivers	*TERT* status
HN 103 PT	54	M	Floor of mouth	SCC	N/A	Y		WT
HN 104 PT	50	F	Mandible	SCC	N/A	Y	TP53	WT
HN 108 PT	49	M	Tongue	SCC	N/A	N		WT
HN 111 PT	45	M	Hard palate	SCC	N/A	Y		WT
HN 112 PT	40	F	Tongue	SCC	N/A	N	FBXW7	WT
HN 115 PT	54	F	Floor of mouth	SCC	N/A	Y	NOTCH1, TP53	WT
HN 116 PT	56	M	Floor of mouth	SCC	N/A	Y		WT
HN 120 PT	46	M	Floor of mouth	SCC	N/A	Y		WT
HN 124 PT	53	M	Tongue	SCC	N/A	Y	CDKN2A	C228T
HN 125 PT	UNK	M	Larynx	SCC	UNK	UNK	TP53	WT
HN 127 PT	52	M	Larynx	SCC	N/A	Y		WT
HN 129 PT	59	M	Supraglottis	SCC	N/A	Y	TP53	WT
HN 133 PT	50	M	Glottis	SCC	N/A	Y	CDKN2A, TP53	WT
HN 134 PT	66	M	Tonsil	SCC	Y	UNK		WT
HN 137 PT	65	M	Tonsil	SCC	Y	Y	FBXW7	WT
HN 138 PT	58	M	Oropharynx/ hypopharynx	SCC	UNK	Y	TP53	WT
HN 139 PT	57	F	Tonsil	SCC	UNK	Y	TP53, NOTCH1	WT
HN 143 PT	49	M	Tonsil	SCC	Y	N		WT
HN 145 PT	58	F	Base of tongue	SCC	Y	UNK		WT
HN 146 PT	44	M	Oropharynx	SCC	UNK	Y		WT
HN 147 PT	72	M	Base of tongue	SCC	UNK	Y		WT
HN 148 PT	46	M	Tonsil	SCC	UNK	Y	NOTCH1	WT
HN 151 PT	54	M	Tonsil	SCC	Y	Y		WT
HN 152 PT	69	F	Tongue	SCC	N/A	Y		C228T
HN 305 PT	50	M	Floor of mouth	SCC	N/A	Y		WT
HN 306 PT1	59	M	Floor of mouth	SCC	N/A	Y		WT
HN01 PT	44	F	Tongue	SCC	N/A	N	TP53	WT
HN02PT-2	64	M	Tongue	SCC	N/A	UNK		C228T
HN03 PT	46	F	Tongue	SCC	N/A	Y		WT
HN04 PT	42	M	Base of tongue	SCC	UNK	N		WT
HN05 PT2	64	F	Alveolar ridge	SCC	N/A	Y		C250T
HN06 PT	72	F	Tongue	SCC	N/A	N		WT
HN07 PT	66	F	Floor of mouth	SCC	N/A	Y		WT
HN08 PT	43	M	Tongue	SCC	N/A	Y		C250T
HN09PT	34	M	Tongue	SCC	N/A	Y	TP53	C228T
HN10PT	82	M	Tongue	SCC	N/A	Y		WT
HN11PT	63	F	Tongue	SCC	N/A	Y	TP53, CDKN2A, HRAS, PIK3CA	WT
HN13PT	71	F	Tongue	SCC	N/A	Y		WT
HN14PT	37	F	Tongue	SCC	N/A	N	TP53, NOTCH1	C228T
HN15PT	67	F	Hard palate	SCC	N/A	Y		WT
HN16PT	63	M	Tongue	SCC	N/A	Y	TP53	WT
HN17PT DNA	65	F	Tonsil	SCC	Y	UNK		WT
HN18PT DNA	59	M	Tonsil	SCC	Y	N		WT
HN19PT DNA	42	M	Tonsil	SCC	Y	N		WT
HN20PT DNA	63	M	Tonsil	SCC	Y	Y		WT
HN21PT DNA	59	M	Tonsil	SCC	N	Y		WT
HN22PT DNA	52	F	Supraglottis	SCC	N/A	Y	TP53, CDKN2A	WT
HN24PT DNA	71	M	Hypopharynx	SCC	N/A	Y	TP53	WT
HN25PT DNA	50	M	Tonsil	SCC	UNK	Y		WT
HN26PT DNA	59	M	Tonsil	SCC	UNK	Y		WT
HN27PT DNA	32	F	Tongue	SCC	N/A	Y	TP53	C228T
HN28PT DNA	70	M	Tonsil	SCC	UNK	N		WT
HN30PT DNA	56	M	Supraglottis	SCC	N/A	N		WT
HN31PT DNA	49	M	Tonsil	SCC	N	N		WT
HN32PT tumor	58	M	Supraglottis	SCC	N/A	Y	TP53	WT
HN33PT tumor	83	M	Floor of mouth	SCC	N/A	Y	TP53, FBXW7	WT
HN34PT tumor	49	M	Base of tongue	SCC	UNK	Y		WT
HN35PT tumor	68	M	Tongue	SCC	N/A	UNK	TP53	WT
HN39PT tumor	44	M	Tonsil	SCC	UNK	Y		WT
HN41PT tumor	42	M	Tonsil	SCC	Y	Y	PIK3CA	WT
HN42PT tumor	56	M	Base of tongue	SCC	Y	N		WT

Table S2. Cont.

Sample ID	Age (y)	Sex	Site/subsite	Histology	HPV status	Tobacco use	Mutations in known drivers	*TERT* status
HN43PT tumor	59	M	Tonsil	SCC	UNK	Y		WT
TUNG 1 PT	35	F	Tongue	SCC	N	N		WT
TUNG 2 PT	51	M	Tongue	SCC	N	N	NOTCH3	WT
TUNG 3 PT	43	F	Tongue	SCC	N	N	NOTCH1	C228T
TUNG 4 PT	45	M	Tongue	SCC	N	N	NOTCH2NL	WT
TUNG 6 PT	45	M	Tongue	SCC	N	N	TP53, NOTCH1, NOTCH2	C228T
TUNG 7 PT	34	F	Tongue	SCC	N	N		C228T

F, female; HPV, human papillomavirus; M, male; N, no; N/A, not applicable; SCC, squamous cell carcinoma; UNK, unknown; Y, yes.

Table S3. *TERT* mutations in glioma subtypes

Glioma subtype	WHO grade	No. of tumors studied	No. of tumors with *TERT* promoter mutation	Tumors with *TERT* mutation (%)
Primary GBM, adult	IV	78	65	83
Primary GBM, pediatric	IV	19	2	11
Astrocytoma	II	8	0	0
Astrocytoma	III	27	4	15
Astrocytoma	IV	5	0	0
Oligodendroglioma	II	19	12	63
Oligodendroglioma	III	26	23	88
Oligoastrocytoma	II	9	2	22
Oligoastrocytoma	III	15	4	27

Other Supporting Information Files

Dataset S1 (XLSX)